FIGURE 1

```
GCTCTCCCTGCTCCAGCAAGGACCATGAGGGCGCTGGAGGGGCCAGGCCTGTCGCTGCTG
                          M  R  A  L  E  G  P  G  L  S  L  L

TGCCTGGTGTTGGCGCTGCCTGCCCTGCTGCCGGTGCCGGCTGTACGCGGAGTGGCAGAA
 C  L  V  L  A  L  P  A  L  L  P  V  P  A  V  R  G  V  A  E

ACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGCGCCCAGTGC
 T  P  T  Y  P  W  R  D  A  E  T  G  E  R  L  V  C  A  Q  C

CCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACGTGTGGCCCG
 P  P  G  T  F  V  Q  R  P  C  R  R  D  S  P  T  T  C  G  P

TGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGCTACTGCAAC
 C  P  P  R  H  Y  T  Q  F  W  N  Y  L  E  R  C  R  Y  C  N

GTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCC
 V  L  C  G  E  R  E  E  E  A  R  A  C  H  A  T  H  N  R  A

TGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCACGCATCGTGT
 C  R  C  R  T  G  F  F  A  H  A  G  F  C  L  E  H  A  S  C

CCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAGAACACGCAGTGCCAGCCG
 P  P  G  A  G  V  I  A  P  G  T  P  S  Q  N  T  Q  C  Q  P

TGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCACCGC
 C  P  P  G  T  F  S  A  S  S  S  S  E  Q  C  Q  P  H  R

AACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTG
 N  C  T  A  L  G  L  A  L  N  V  P  G  S  S  S  H  D  T  L

TGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAG
 C  T  S  C  T  G  F  P  L  S  T  R  V  P  G  A  E  E  C  E

CGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTGCAGCGGCTG
 R  A  V  I  D  F  V  A  F  Q  D  I  S  I  K  R  L  Q  R  L

CTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGCCGCGCGGCC
 L  Q  A  L  E  A  P  E  G  W  G  P  T  P  R  A  G  R  A  A

TTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGACGGGGCGCTG
 L  Q  L  K  L  R  R  R  L  T  E  L  L  G  A  Q  D  G  A  L

CTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAGCGGAGCGTC
 L  V  R  L  L  Q  A  L  R  V  A  R  M  P  G  L  E  R  S  V

CGTGAGCGCTTCCTCCCTGTGCACTGATCCTGGCCCCCTCTTATTTATTCTACATCCTTG
 R  E  R  F  L  P  V  H  *

GCACCCCACTTGCACTGAAAGAGGCTTTTTTTTAAATAGAAGAAATGAGGTTTCTTAAAG

CTTATTTTTATAAAGCTTTTTCATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
```

FIGURE 2

TGGCATGTCGGTCAGGCACAGCAGGGTCCTGTGTCCGCGCTGAGCCGCGCTCTCCCTGCT

CCAGCAAGGACCATGAGGGCGCTGGAGGGGCCAGGCCTGTCGCTGCTGTGCCTGGTGTTG
      M R A L E G P G L S L L C L V L

GCGCTGCCTGCCCTGCTGCCGGTGCCGGCTGTACGCGGAGTGGCAGAAACACCCACCTAC
A L P A L L P V P A V R G V A E T P T Y

CCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGCGCCCAGTGCCCCCCAGGCACC
P W R D A E T G E R L V C A Q C P P G T

TTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGC
F V Q R P C R R D S P T T C G P C P P R

CACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGG
H Y T Q F W N Y L E R C R Y C N V L C G

GAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGC
E R E E E A R A C H A T H N R A C R C R

ACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCC
T G F F A H A G F C L E H A S C P P G A

GGCGTGATTGCCCCGGGTGAGAGCTGGGCGAGGGGAGGGGCCCCCAGGAGTGGTGGCCGG
G V I A P G E S W A R G G A P R S G G R

AGGTGTGGCAGGGGTCAGGTTGCTGGTCCCAGCCTTGCACCCTGAGCTAGGACACCAGTT
R C G R G Q V A G P S L A P *

CCCCTGACCCTGTTCTTCCCTCCTGGCTGCAGGCACCCCCAGCCAGAACACGCAGTGCCA

GCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCA

CCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACAC

CCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGTGAGCCAGAGGC

CTGAGGGGGCAGCACACTGCAGGCCAGGCCCACTTGTGCCCTCACTCCTGCCCCTGCACG

TGCATCTAGCCTGAGGCATGCCAGCTGGCTCTGGGAAGGGGCCACAGTGGATTTGAGGGG

TCAGGGGTCCCTCCACTAGATCCCCACCAAGTCTGCCCTCTCAGGGGTGGCTGAGAATTT

GGATCTGAGCCAGGGCACAGCCTCCCCTGGAGAGCTCTGGGAAAGTGGGCAGCAATCTCC

FIGURE 2 (continued)

TAACTGCCCGAGGGGAAGGTGGCTGGCTCCTCTGACACGGGGAAACCGAGGCCTGATGGT

AACTCTCCTAACTGCCTGAGAGGAAGGTGGCTGCCTCCTCTGACATGGGGAAACCGAGGC

CCAATGTTAACCACTGTTGAGAAGTCACAGGGGGAAGTGACCCCCTTAACATCAAGTCAG

GTCCGGTCCATCTGCAGGTCCCAACTCGCCCCTTCCGATGGCCCAGGAGCCCCAAGCCCT

TGCCTGGGCCCCCTTGCCTCTTGCAGCCAAGGTCCGAGTGGCCGCTCCTGCCCCCTAGGC

CTTTGCTCCAGCTCTCTGACCGAAGGCTCCTGCCCCTTCTCCAGTCCCCATCGTTGCACT

GCCCTCTCCAGCACGGCTCACTGCACAGGGATTTCTCTCTCCTGCAAACCCCCCGAGTGG

GGCCCAGAAAGCAGGGTACCTGGCAGCCCCCGCCAGTGTGTGTGGGTGAAATGATCGGAC

CGCTGCCTCCCCACCCCACTGCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTG

TGGCTTTCCAGGACATCTCCATCAAGAGGAGCGGCTGCTGCAGGCCC

FIGURE 3

FIGURE 3 (continued)

FIGURE 3 (continued)

```
198 -  -  QIENVKGTEDSGTTVLLPLVIFFG-L-  -  -          TNFR1
212 GAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPA        TNFR2
200 TPPEGSDSTAPSTQEPEAPPEQDLIAST-  -  -VAGVTTV       NFR
224 LAILLS-  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  LHR
159 -  -  -LTSNTKCKEEGSRSNL-  -  -  -  -  -  -GWL-  -  -   FAS
130 -  -ARSSQALSPHPQPTHLPYVSEMLEAR-  -TAGHQTL         CD27
204 AASKLTRAPDSPSSVGRPSSDPGLSPTQP-  -CPEGSGDCR        CD30
194 ALVVIP-  -  -  -  -  -  -  -  -  -  -  -CPEGSGDCR         CD40
164 DLSPGASSVTPPAPAREPGHSPQIIS-  -  -  -  -  -  -       4-1BB
169 -  -RDPPATOPQETOGPP-  -  -  -  -  -  -  -           CD40
200 -  -GLSESILT-  -  -  -  SELTITMNHTDCN               VC22
200 -  -GLSESIST-  -  -  -  SELTITMNHKDCD               CR8

196 -  -  -  CTGF-  -PLSTRVPG                          TNFR-6a
143 -  -  -  -  -  -                                    TNFR-6b


  7 EGSTGDFAL-  -  -  -  -  -  -  -  -  -CLLSLFIGLMY-  -  -    TNFR1
    MGSSQPVVTRGTTDNLIPVYCS-  -PVGLIVGVTALGLLIIGVV            TNFR2
    L-  -  -  -  -  -  -  -  -  -  -  -  -VLFLFFTVLACAWMRHPS    NFR
178 -  -  -  -  -  -  -  -  -  -CLL-LFPIPLIV-  -  -            LHR
164 AD-  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -            FAS
242 KQCEPDYLDEAGRCTACVSCSRDD-VEKTPCAWNSSRTC                 CD27
200 -  -  -I-  -  -  -  -  -  -  -  -IFGIGFAILLVLVFIKK-  -     CD30
190 -  -  -  FFL-  -  -  -  -  -  -  -  -  -  -  -  -           CD40
184 -  -  -ARPITVQPTEA-  -  -  -  -  -  -  -  -  -             4-1BB
221 PVFREEY-  -  -  -  -  -FSV-NKVATSGFFTGENR                VC22
221 PVFRNGY-  -  -  -  -  -FSV-NEVATSGFFTGQNR                CR8

208 AEECER-  -  -  -  -  -  -  -  -  -  -  -  A V I         TNFR-6a
143 -  -  -  -  -  -  -  -  -  -  -  -  -  -  -              TNFR-6b


235 -  -  -  -  -  -  -  -  -  -RYQRW-  SKLYSI-  -  -  VCGKSTPEKEGELEGTT   TNFR1
280 NCV-  -  -  -IMTQVK-KKPLC-  -  -  -  -  -  -  -  -  -       TNFR2
269 -  -  -  -  -  -YIAFKRWNSCKQ-  -  -  -  -  -  -  -  -       NFR
250 LCR-  -  KLGTLLKRH-  -  -  -  -  -  -  -  -  -  -  -       LHR
189 -  -  -  -  -  WVRRKEVQK-  -  -  -  -  -  -  -  -  -       FAS
166 -  -  -  -  -  FRQ-  -  -  -  TCRKHRKENQGSHE-  -  -         CD27
282 ECRPGHICATSATNSCARCVPYPICAAETVTKPQDMAEKD               CD30
166 -  -  -  -  -  FRQ-  -  -  -  -  -  -  -  -  -  -           CD40
246 -  -  -  -  -  VAKK-  -  -  -  -  -  -  -  -  -            4-1BB
246 -  -  -  -  -  -WP-  -R-  -  -  -  -  -  -  -  -            CD40
246 -  -  -  -  -  YONISK-  VCT-  -  -  -  -  -  -  -           VC22
246 -  -  -  -  -  YONISK-  VCT-  -  -  -  -  -  -  -           CR8

217 DFV-  -  AFQDISIKR-  -  -  -  -  -  -  -  -  -  -           TNFR-6a
143 -  -  -  -  -  -  -  -  -  -  -  -  -  -  -              TNFR-6b
```

```
264 TKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYTPGD- TNFR1
294 -----LQREAKVPHLPA-DKARGTQGPEQHLLITA-      TNFR2
281 -----NKQGANSRPV-NQTPPEGEKLHSDGISVD        NGFR
262 -----PEGEESPPCPA-PRADPHFPDLAEPLL----      LTBR
212 ---SPTLNPE--TVAINLSDVDLSKYITT-----        FAS
169 -----------------------------LP---        CD27
322 TTFEAPPLGEQPDCNPTPE-NGEAPASTPTQSLLVDSQA   CD30
222 -----PTNKAPHPKQE-PQ-EINFPD-----           CD40
193 ---------------------------------         4-1BB
198 ----TSQPSTRPV-E---VPGGRAVAAILGLGL-        OX40
255 ----LNFEIKCNN------KGS--SFKQ--LTK--       VC22
255 ----LNFEIKCNN------KDSYSSSKQ--LTK--       CR38

229 ---LQRLLQALEAPE-GW--GP--T-                TNFR-6a
143 ---E-SWARGG-------A-                      TNFR-6b

'04 --CPNFAAPRREVAPPYQGADPILATA-              TNFR1
1   --PSSSSSSLESSASAL-                        TNFR2
    SQSLHDQPHTQTASGQALK--GDGLYSSLPPAKREE      NGFR
    PMSGDLSPSPAGPPT---IAGV-                   LTBR
236 ARTLSTHWPQRSLCSDFI--RILVIFSGHFLVFTLA      FAS
171 SKTLPIPTSAPVALSSTGKPVLDAGPVLFWVILVLVVVG   CD27
361 DLPGSNTAAPV-                              CD30
241 ALTSTALLFL-                               CD40
193 VLGLL-                                    4-1BB
193 GPLAILALYLLRRDQ-                          OX40
224 LFFLTLRFSVVKR-                            VC22
274 AKNDDG-M-                                 CR38
276 TKNDDDSI-

246 --PRAGRAALQLK--L-                         TNFR-6a
151 --PRSG-                                   TNFR-6b

329 ---LASDPIPNPLQKWEDSAHKPQSLDTDDPATLYAVVE   TNFR1
339 ---DRRAPTRNQPQAPGVEASGAGEARASTGSSDSS      TNFR2
347 VEKLL---APSLEEVLQQQSPL----NGS-            NGFR
303 ---MTLSQV------VQAREL--EAE-               LTBR
240 GALFL------HQ-                            FAS
207 SSAFLLCHRRACRKRIRQKLHLCYPVQTSQPKLELVDSRP  CD27
401 ---QETL-                                  CD30
72  GRKKLL-                                   4-1BB
281 ---MSHSETVTLAGDCLSSVDIYILYSNTN            OX40
284 ---MPHSESVTLVGDCLSSVDIYILYSNTN            VC22
258 ---RRRLTELLGAQDGALLVRLLQALR-              TNFR-6a
155 ---                                       TNFR-6b
```

FIGURE 3 (continued)

FIGURE 3 (continued)

365 NVPPLRWKEFVRRLGLSDHEIDRLELQNGRCLREAQYSML —————— TNFR1
372 PGGHGTQVNVTCIV[N]VCSSSDH-SSQCSSQASSTMGDT- —————— TNFR2
355 AGDTWRHLAG[E]LGYQPEHID[S]FTHEACPVR---ALL —————— NFR
327 PGEHGQVAHG[A]NGIH[V]GGSVTVTGNIYINYGPVLGGT- —————— LTBR
246 ----KGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLL —————— LTBR
214 -----RRKYRSNKGESPVEPAEPCRYSCPR-------- —————— FAS
441 RRSSTQLRS[G]AS[V]TEPVAEERGLMSQPLMETCHSVGAAYL —————— CD27
256 ----HG[C]QPVT- —————— CD30
222 --------- —————— CD40
245 ----RLPPD-AHKPP[G]GSF- —————— 4-1BB
308 AQDYETDTISYR[V]GN[V]LDD[D]SHMPGSNIHK- —————— OX40
311 TQDYETDTISYH[V]GN[V]LDV[D]SHMPGRCDTHK- —————— VC22
202 ------[V]ARHP[G]LER- —————— CR8
155 ------[G]RRC[G]RGQ- —————— TNFR-6a
     —————— TNFR-6b

405 ATWRRTPRREATLELLGRVLRDMDLLGC- —————— TNFR1
/ -DSSPSES-PKDE----QVPFSKEECAF- —————— TNFR2
    ASWATQDSATLDA-
279 -RGPGDP-PAPP----EPPYPTPEEGA- —————— NFR
219 RNWHQLHGKKEA-YDTLIKDLKKANL--CTLAEKIQ- —————— LTBR
481 ESLPLQDASPAGG-PSSPRDLPEPRVSTEHTNNKIEKIYI- —————— FAS
261 PSSPRDLPEPRVSTEHTNNKIEKIYI- —————— CD27
222 --------- —————— CD30
260 --------- —————— CD40
339 ----YI —————— 4-1BB
342 -PITNSK- —————— OX40
163 LITNSNSQY- —————— VC22
291 --------- —————— CR8
     —————— TNFR-6a
     —————— TNFR-6b

434 ---------LEDIEEALCGPAALP- —————— TNFR1
431 -----RSQLETPETLLGSTEEK- —————— TNFR2
401 ------LLAALRRIQRADNFR- —————— NFR
386 TIILKDITSD-SENSNFR- —————— LTBR
312 -----PGPSELSTPYQEDGKAW LTBR
246 FAS
520 NKADTVIVGTVKAELPEGRGLAGPAEPELEEELEADHTPH-P CD27
FK- —————— CD30
351 ------QEDGKES CD40
345 ------QPFHRPVQTT 4-1BB
   PTHF- OX40
   PTRF- VC22
   RTP CR8
291 SVRER TNFR-6a
161 VAGPS TNFR-6b

FIGURE 3 (continued)

```
449 - - - - - - - - - - - - - - - - - - - - - - - PAPSLLR                          TNFR1
448 P - - - - - - - - - - - - LPLGVPDAGMKPS                                          TNFR2
413 L V E S L C S E S - - - - - - - - - TATSPV                                       NGFR
403 H - - - - - - - - - LAET-ETLGCQDL                                                LNR
329 - - - - - - - - - - - - - - - - NEIQSLV                                          FAS
247 I Q E D - Y R K P - - - - - - - - EPACSP                                         CD27
560 Y P E Q E T E P P L G S C S D V M L S V E E G K E D P L P T A A S G K             CD30
270 R - - - - - - - - - - - - ISVQ-ERQ                                               CD40
236 Q E E D G C - - - S C - - R P E E E G - - - - - G C E L                          4-1BB
263 I Q E E Q A D A H - - - - STLAKI                                                 OX40
349 - - - - - - - - - - - - - - - - L                                               VC22
355 - - - - - - - - - - - - - - - - L                                               CR~B

296 F - - - - - - - - - - - LPV - - - - - H                                          TNFR-6a
168 L - - - - - - - - - - - AP                                                       TNFR-6b
```
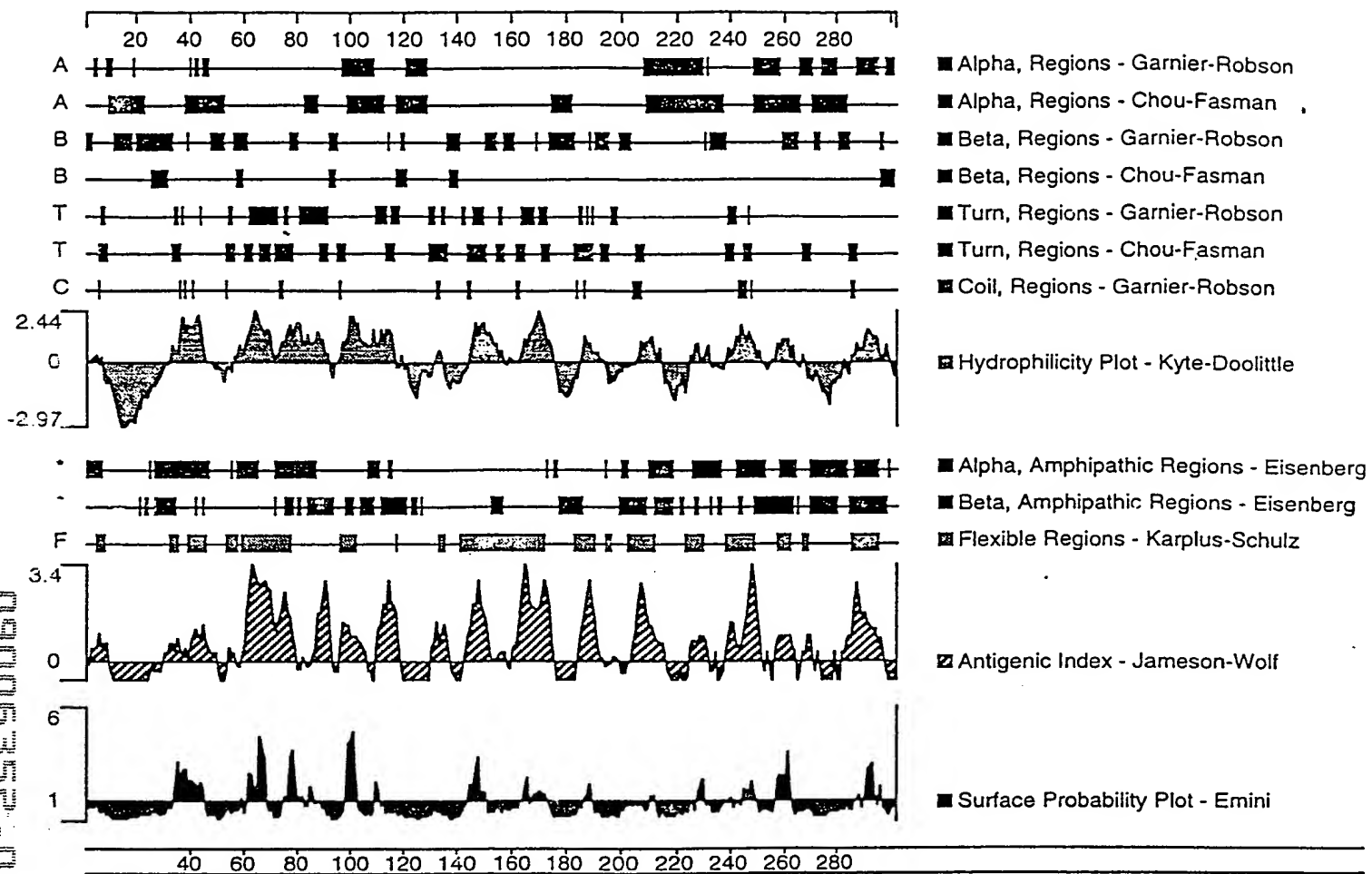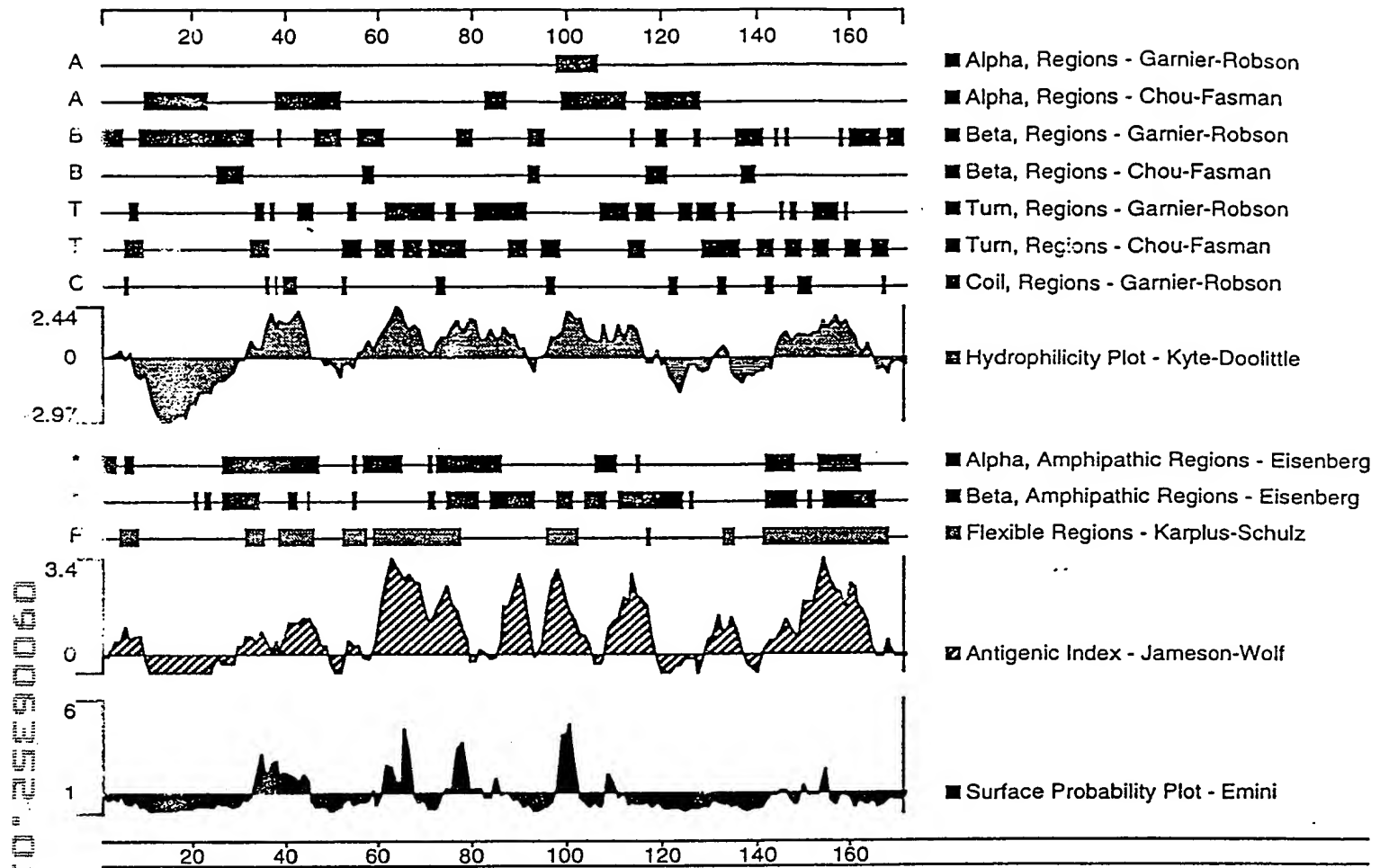
FIGURE 4

FIGURE 5

FIGURE 6

HELDIO6R
```
GGCACGAGCA GGGTCCTGTN TCCGCCCTGA GCCGCGCTCT NCCTGCTCCA GCAAGGACCA
TGAGGGCGCT GGAGGGGCCA GGCCTGTCGC TGCTGTGCCT GGTGTTGGCG CTGCCTGCCC
TGCTGCCGGT GCCGGCTGTA CGCGGAGTGG CAGAAACACN NACNTACCCC TGGCGGGACG
NAGAGACAGG GGAGCGGCTG GTGTNTNCCC ANTGCCCCCC AGGCACCTTT NTGCAGCGGC
CGTGCCGNCG AGACAGCCCC ACGACGTGTG GCCCGTNTCC ACCGCGCCAC TACACGCATT
CTGGAACTAC CTGGAGCGCT GNCGTTACTN CAACGTCCTC TGCGGGGAGC GTNAGGAGGA
GGCACGGGTT TNCCACGNCA ACCACAACCG NGGNTTACCG TNGCCGNACC GGTTTCTTCG
NGGCAAGTTG GTTTTTNNTT TGGAGNAAGG ATTCGTGTTN CAATTNATTG ACGNAGTGAT
TNNNCNCGGG AAACTNAAA
```

HCEOW38R
```
CGCAACTGCA CGGCCCTGGG ACTGGCCCTC AATGTGCCAG GNTCTTCCTC CCATGACACC
CTGTGCACCA GCTGCACTGG CTTCCCCCTC AGCACCAGGG TACCANGAGC TGAGGAGTGT
GAGCNTGCCG TCATCGACTT TTTGGCTTTC CAGGACATCT CCATCAAGAG GCTGCAGCGG
CTGCTCANGC C
```